Amendments to the Specification:

Please replace the paragraph at page 8, from line 14 through line 15, with the following paragraph:

-- 7B Amino acid sequence alignment of example wild-type Archaeal DNA polymerases according to one embodiment of the invention: Pfu: SEQ ID NO: 27; Tgo: SEQ ID NO: 29; KOD: SEQ ID NO: 30; Vent: SEQ ID NO: 31; Deep: SEQ ID NO: 28; JDF-3: SEQ ID NO: 32. --

Please replace the paragraph at page 73, from line 16 through line 26 with the following paragraph:

-- To analyze Tgo, Pfu, KOD, JDF-3 mutant proteins, the DNA sequence encoding each of Tgo, Pfu, KOD, and JDF-3 DNA polymerases is PCR amplified using primers GGG AAA **CAT ATG** ATC CTT GAC GTT GAT TAC (SEQ ID NO: 109; where NdeI site in bold and start codon underlined) and GGG AAA **GGA TCC** TCA CTT CTT CTT CCC CTT C (SEQ ID NO: 110; where BamHI site shown in bold type). The PCR products are digested, purified, and ligated into a high expression level vector using standard methods. Plasmid clones are transformed into BL21(DE3). Recombinant bacterial clones are grown using standard procedures and polymerase mutants are expressed in the absence of induction. The exonuclease and polymerase activities of recombinant clones are assayed using bacterial lysates. Typically, crude extracts are heated at 70°C for 15-30 minutes and then centrifuged to obtain a cleared lysate. --

Respectfully submitted,

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